

From: Romeo, David
Sent: Sunday, January 09, 2005 7:46 AM
To: STIC-Biotech/ChemLib
Subject: 10028051

Requester's Name: ... David Romeo
Serial Number: ... 10028051
Art Unit: ... 1647
Office: ... REM 4D39
Mailbox: ... REM 4C70
Phone: ... 571 272-0890
Date of Request: ... 01/09/05

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PLEASE PROVIDE RESULTS ON DISK(s)

Search the commercial/public and interference files for SEQ ID NO: 1.

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STAFF USE ONLY

Searcher: ED HART
Searcher Phone: 2-
Date Searcher Picked up: 1/10/05
Date Completed: 1/11/05
Searcher Prep/Rev. Time: 1/11/05
Online Time: _____

Type of Search

NA Sequence: # 3
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: Q16P
WWW/Internet: _____
Other(Specify): _____

OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 9805.83 Seconds
(without alignments)
1148.874 Million cell updates/sec

Title: US-10-028-051A-1

Perfect score: 2374

Sequence: 1 aatagatgcgcgcgcgcacg.....aaaaaaaaaaaaaaaaaa 2374

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*
1: gb_pa:*
2: gb_htg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_otc:*
12: gb_ey:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2335	98.4	2351	4	BTU24164
2	1467.4	61.8	2039	6	ARI29187
3	1467.4	61.8	2039	6	AR447852
4	1399.6	59.0	1920	6	BD192740
5	1384.6	58.3	1909	6	AX329773
6	1384.6	58.0	1893	6	HSU1903
7	1376.4	58.0	1893	6	ARI16408
8	1376.4	58.0	1893	6	BD195148
9	1376.4	58.0	1893	6	HSU68057
10	1122.8	47.3	1476	6	AX565712
11	1122.8	47.3	1476	6	AX597112
12	1122.8	47.3	1476	6	AX701367
13	1122.8	47.3	1476	6	AX821908
14	1122.8	47.3	1476	6	HSU24163
15	1082.4	45.6	2814	10	BC016884
16	1070	45.1	2540	10	MMU88568
17	1055.2	44.4	1687	9	AK130009
18	1054.4	44.4	1363	9	BC027855
19	1034.2	43.6	2176	6	ARI16407

20	1034.2	43.6	2176	6	AX305981	AX305981 Sequence
21	1034.2	43.6	2176	10	MMU68058	U68058 Mus musculus
22	1031	43.4	2176	6	BD195147	BD195147 Endoderm,
23	831.8	35.0	1786	10	MMU91905	U91905 Mus musculus
24	676.6	28.5	124720	9	AC105396	AC105396 Homo sapi
25	672.8	28.3	1833	5	AF218057	AF218057 Gallus ga
26	654.6	27.6	207061	2	AC012552	AC012552 Homo sapi
27	607.2	25.6	1076	10	MAU91904	U91904 Mesocricetu
28	589	24.8	97944	9	AC108514	AC108514 Homo sapi
29	587	24.7	725	6	CQ719712	CQ719712 Sequence
30	481.6	20.3	640	5	AF207665	AF207665 Gallus ga
31	463.8	19.5	1867	5	BC074538	BC074538 Xenopus t
32	452.8	19.1	67845	2	AC016315	AC016315 Homo sapi
33	452	19.0	1291	5	XLU78598	U78598 Xenopus lae
34	447	18.8	190906	10	AL928578	AL928578 Mouse DNA
35	447	18.8	250663	2	AC134905	AC134905 Mus muscu
36	446	18.8	1875	5	U68059	U68059 Xenopus lae
37	446	18.8	1875	6	ARI16405	ARI16405 Sequence
38	446	18.8	1875	6	BD195145	BD195145 Endoderm,
39	420.8	17.7	611	11	BV099134	BV099134 RPAWSEGO
40	420.8	17.7	611	11	BV158572	BV158572 RPAWSEGO
41	415.4	17.5	238965	2	AC126647	AC126647 Rattus no
42	414.6	17.5	487	6	CQ691410	CQ691410 Sequence
43	413.6	17.4	1434	5	XLUJ3304	AU009304 Xenopus l
44	397.6	16.7	948	5	AF116853	AF116853 Danio rer
45	358.6	15.1	391	4	AB073103	AB073103 Oryctolag

OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 1036 Seconds
(without alignments)
12029.047 Million cell updates/sec

Title: US-10-028-051A-1

Perfect score: 2374

Sequence: 1 aatagatgcgcgcgcgcacg.....aaaaaaaaaaaaaaaaaa 2374

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N GeneSeq_23Sep04:*
1: GeneSeqn1980a:*
2: GeneSeqn1990a:*
3: GeneSeqn2000a:*
4: GeneSeqn2001a:*
5: GeneSeqn2001ba:*
6: GeneSeqn2002a:*
7: GeneSeqn2002ba:*
8: GeneSeqn2003a:*
9: GeneSeqn2003ba:*
10: GeneSeqn2003ca:*
11: GeneSeqn2003da:*
12: GeneSeqn2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Maximum DB seq length: 200000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
Issued Patents_NA:*

1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:**
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:**
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:**
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:**
5: /cgn2_6/ptodata/1/ina/PCITUS_COMB.seq:**
6: /cgn2_6/ptodata/1/ina/backfile1.seq:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1467.4	61.8	2039	3	US-09-376-531-45	Sequence 45, Appl
2	1467.4	61.8	2039	4	US-09-376-594-478	Sequence 478, Appl
3	1376.4	58.0	1893	3	US-08-878-474-10	Sequence 10, Appl
4	1034.2	43.6	2176	3	US-08-878-474-8	Sequence 8, Appl
5	446	18.8	1875	3	US-08-878-474-4	Sequence 4, Appl
6	308.6	13.0	2009	3	US-09-376-531-108	Sequence 108, Appl
7	209.4	8.8	246	4	US-09-016-434-103	Sequence 103, Appl
8	72	3.0	401	4	US-09-643-597-277	Sequence 277, Appl
9	72	3.0	401	4	US-09-480-884-277	Sequence 277, Appl
10	72	3.0	401	4	US-09-542-615-277	Sequence 277, Appl
11	72	3.0	401	4	US-09-606-421-277	Sequence 277, Appl
12	72	3.0	401	4	US-09-630-940-277	Sequence 277, Appl
13	61.4	2.6	588	4	US-09-546-043-10	Sequence 10, Appl
14	61.4	2.6	1984	4	US-08-937-067-5	Sequence 5, Appl
15	58.4	2.5	741	4	US-09-546-043-11	Sequence 11, Appl
16	58.4	2.5	804	4	US-09-546-043-12	Sequence 12, Appl
17	58.4	2.5	942	4	US-09-546-043-2	Sequence 2, Appl
18	58.4	2.5	1017	4	US-09-546-043-9	Sequence 9, Appl
19	58.4	2.5	2075	4	US-09-087-031E-2	Sequence 2, Appl
20	58.4	2.5	2075	4	US-09-546-043-1	Sequence 1, Appl
21	58.4	2.5	2075	4	US-09-514-885-2	Sequence 2, Appl
22	58.4	2.5	2078	4	US-09-087-031E-1	Sequence 1, Appl
23	58.4	2.5	4245	3	US-09-276-531-16	Sequence 16, Appl
24	58.4	2.5	4500	4	US-09-087-031E-27	Sequence 27, Appl
25	56.8	2.4	1308	4	US-08-937-067-18	Sequence 18, Appl
26	55.2	2.3	1869	4	US-09-148-545-56	Sequence 56, Appl
27	54.6	2.3	870	4	US-08-937-067-3	Sequence 3, Appl

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
C	1	1467.4	61.8	2039	3	US-09-276-531-45	Sequence 45, Appl
	2	1467.4	61.8	2039	4	US-09-976-594-478	Sequence 478, Appl
	3	1376.4	58.0	1893	3	US-08-878-474-10	Sequence 10, Appl
	4	1034.2	43.6	2176	3	US-08-878-474-8	Sequence 8, Appl
	5	446	18.8	1875	3	US-08-878-474-4	Sequence 4, Appl
	6	308.6	13.0	2009	3	US-09-276-531-108	Sequence 108, Appl
	7	209.4	8.8	246	4	US-09-016-434-103	Sequence 103, Appl
	8	72	3.0	401	4	US-09-643-597-277	Sequence 277, Appl
	9	72	3.0	401	4	US-09-480-884-277	Sequence 277, Appl
	10	72	3.0	401	4	US-09-542-615A-277	Sequence 277, Appl
	11	72	3.0	401	4	US-09-606-422B-277	Sequence 277, Appl
	12	72	3.0	401	4	US-09-630-940B-277	Sequence 277, Appl
	13	61.4	2.6	588	4	US-09-546-063-10	Sequence 10, Appl
	14	61.4	2.6	1984	4	US-08-937-067-5	Sequence 5, Appl
	15	58.4	2.5	741	4	US-09-546-063-11	Sequence 11, Appl
	16	58.4	2.5	804	4	US-09-546-043-12	Sequence 12, Appl
	17	58.4	2.5	942	4	US-09-546-043-2	Sequence 2, Appl
	18	58.4	2.5	1017	4	US-09-546-043-9	Sequence 9, Appl
	19	58.4	2.5	2075	4	US-09-087-031E-2	Sequence 2, Appl
	20	58.4	2.5	2075	4	US-09-546-043-1	Sequence 1, Appl
	21	58.4	2.5	2075	4	US-09-514-885-2	Sequence 2, Appl
	22	58.4	2.5	2078	4	US-09-087-031E-1	Sequence 1, Appl
	23	58.4	2.5	4245	3	US-09-276-531-16	Sequence 16, Appl
	24	58.4	2.5	4500	4	US-09-087-031E-27	Sequence 27, Appl
	25	56.8	2.4	1308	4	US-08-937-067-18	Sequence 18, Appl
	26	55.2	2.3	1869	4	US-09-148-545-56	Sequence 56, Appl
	27	54.6	2.3	870	4	US-08-937-067-3	Sequence 3, Appl
	28	54.6	2.3	1960	4	US-09-148-545-114	Sequence 114, Appl
	29	54.4	2.3	1141	4	US-09-806-708B-22	Sequence 22, Appl
	30	49.4	2.1	7218	1	US-08-332-463-14	Sequence 14, Appl
	31	49.2	2.1	2030	4	US-08-937-067-1	Sequence 1, Appl
	32	45.2	1.9	2134	4	US-09-087-031E-26	Sequence 26, Appl
	33	45	1.9	221	4	US-09-621-976-13585	Sequence 13585, A
	34	45	1.9	1796	3	US-09-276-531-113	Sequence 113, Appl
	35	45	1.9	2186	4	US-09-360-545-66	Sequence 66, Appl
	36	44.4	1.9	1305	4	US-08-815-783-3	Sequence 3, Appl
	37	44.4	1.9	1430	4	US-09-157-864-3	Sequence 3, Appl
	38	44.2	1.9	1141	4	US-09-806-708B-22	Sequence 22, Appl
	39	44.2	1.9	11558	5	PCT-US93-06251-23	Sequence 23, Appl
	40	44	1.9	1401	4	US-09-252-991A-14814	Sequence 14814, A
	41	44	1.9	1908	4	US-09-352-991A-15075	Sequence 15075, A
	42	44	1.9	3900	4	US-09-352-991A-14550	Sequence 14550, A
	43	43.6	1.8	1383	4	US-09-735-846-1	Sequence 1, Appl
	44	43.4	1.8	7218	1	US-08-332-463-14	Sequence 14, Appl
	45	43.2	1.8	1008	4	US-09-780-644-1	Sequence 1, Appl

OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 2258.27 Seconds
(without alignments)
6031.844 Million cell updates/sec

Title: US-10-028-051A-1

Perfect score: 2374
Sequence: 1 aatagatgcgcgcgcag.....aaaaaaaaaaaaaaaaaa 2374

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4293498 seqs, 2868903791 residues

Total number of hits satisfying chosen parameters: 8586996

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: /cgn2_6/ptcodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptcodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptcodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptcodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptcodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptcodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptcodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptcodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptcodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptcodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptcodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptcodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptcodata/1/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptcodata/1/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptcodata/1/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptcodata/1/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptcodata/1/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptcodata/1/pubpna/US10_NEW_PUB.seq:*
- 19: /cgn2_6/ptcodata/1/pubpna/US11_NEW_PUB.seq:*
- 20: /cgn2_6/ptcodata/1/pubpna/US60_NEW_PUB.seq:*
- 21: /cgn2_6/ptcodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2374	100.0	2374	13	US-10-028-051-1
2	2374	100.0	2374	14	US-10-090-049-1
3	2374	100.0	2374	15	US-10-014-055-1
4	1493	62.9	2625	16	US-10-062-674-1395
5	1467.4	61.8	2039	9	US-09-974-298-16
6	1384.6	58.3	1909	10	US-09-960-706-989
7	1384.6	58.3	1909	10	US-09-873-319-645
8	1384.6	58.3	1909	10	US-09-873-367C-282
9	1376.4	58.0	1893	9	US-09-903-180B-10
10	1376.4	58.0	1893	9	US-09-903-187A-10
11	1376.4	58.0	1893	9	US-09-903-171A-10
12	1376.4	58.0	1893	9	US-09-903-188A-10
13	1376.4	58.0	1893	9	US-09-903-323A-10
14	1376.4	58.0	1893	9	US-09-903-325A-10
15	1376.4	58.0	1893	9	US-09-903-170C-10
16	1124.4	47.4	1484	13	US-10-028-051-3
17	1124.4	47.4	1484	14	US-10-090-049-3

18	1124.4	47.4	1484	15	US-10-014-055-3	Sequence 3, Appli
19	1122.8	47.3	1476	15	US-10-172-118-614	Sequence 614, App
20	1122.8	47.3	1476	16	US-10-342-887-614	Sequence 614, App
21	1034.2	43.6	2176	9	US-09-903-180B-8	Sequence 8, Appli
22	1034.2	43.6	2176	9	US-09-903-187A-8	Sequence 8, Appli
23	1034.2	43.6	2176	9	US-09-903-171A-8	Sequence 8, Appli
24	1034.2	43.6	2176	9	US-09-903-188A-8	Sequence 8, Appli
25	1034.2	43.6	2176	9	US-09-903-323A-8	Sequence 8, Appli
26	1034.2	43.6	2176	9	US-09-903-325A-8	Sequence 8, Appli
27	1034.2	43.6	2176	9	US-09-903-170C-8	Sequence 8, Appli
28	452	19.0	1291	13	US-10-028-051-23	Sequence 23, Appl
29	452	19.0	1291	14	US-10-090-049-23	Sequence 23, Appl
30	452	19.0	1291	15	US-10-014-055-23	Sequence 23, Appl
31	446	18.8	1875	9	US-09-903-180B-4	Sequence 4, Appli
32	446	18.8	1875	9	US-09-903-187A-4	Sequence 4, Appli
33	446	18.8	1875	9	US-09-903-171A-4	Sequence 4, Appli
34	446	18.8	1875	9	US-09-903-188A-4	Sequence 4, Appli
35	446	18.8	1875	9	US-09-903-323A-4	Sequence 4, Appli
36	446	18.8	1875	9	US-09-903-325A-4	Sequence 4, Appli
37	446	18.8	1875	9	US-09-903-170C-4	Sequence 4, Appli
38	414.6	17.5	487	16	US-10-242-535A-36336	Sequence 36336, A
39	414.6	17.5	487	16	US-10-085-783A-36336	Sequence 36336, A
40	394	16.6	475	10	US-09-918-995-859	Sequence 859, App
41	377.4	15.9	512	16	US-10-062-674-230	Sequence 230, App
42	333.2	14.0	574	16	US-10-242-535A-14020	Sequence 14020, A
43	333.2	14.0	574	16	US-10-085-783A-14020	Sequence 14020, A
44	325.2	13.7	492	15	US-10-102-524-1581	Sequence 1581, Ap
45	311.4	13.1	472	16	US-10-242-535A-42387	Sequence 42387, A

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OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 6773.9 Seconds
(without alignments)
12770.772 Million cell updates/sec

Title: US-10-028-051A-1

Perfect score: 2374
Sequence: 1 aatagatgcgcgcgcag.....aaaaaaaaaaaaaaaaaa 2374

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hic:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_ges1:*
- 9: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1403.6	59.1	1891	3	CR622855	full-1 leng
2	1319.4	55.6	1780	3	CR620343	full-1 leng
3	1089.6	45.9	2922	3	AK029941	Mus muscu
4	1084.6	45.7	2390	3	AK019093	Mus muscu
5	1038.2	43.7	1305	3	CR593578	full-1 leng
6	889.8	37.5	1159	1	AL515416	AL515416
7	818	34.5	1094	1	AL528836	AL528836
8	817.4	34.4	1032	1	AL546734	AL546734
9	805.8	33.9	1001	1	AL548498	AL548498
10	774.6	32.6	1065	7	U69182	U69182
11	752.6	31.7	928	1	AL527859	AL527859
12	748.4	31.5	750	7	CK775692	966826 MA
13	745.8	31.4	1051	1	AL573040	AL573040
14	740.2	31.2	991	1	AL526385	AL526385
15	720.6	30.4	891	6	CD105319	AGENCOURT
16	704.8	29.7	747	7	CR453950	CR453950
17	661	27.8	797	9	AY410028	Homo sapi
18	651	27.4	835	4	BI913036	BI913036
19	644.8	27.2	728	4	BI832471	BI832471
20	642.2	27.1	787	1	AU141161	AU141161
21	640.6	27.0	1043	5	BX459201	BX459201
22	638.4	26.9	730	5	BP147378	BP147378
23	638.2	26.9	745	5	BP148017	BP148017
24	635.8	26.8	719	7	CN315376	CN315376
25	629.4	26.5	712	5	BX955693	BX955693
26	622	26.2	805	4	BP455757	BP455757
27	617.8	26.0	714	5	BP455757	BP455757
28	608.8	25.6	1010	1	AL526570	AL526570
29	608.2	25.6	797	9	AY410030	Mus muscu
30	601.6	25.3	829	7	CF411660	CF411660
31	596.2	25.1	1106	1	AL546699	AL546699
32	592.2	24.9	678	2	AW160750	AW160750
33	591.6	24.9	797	9	AY410029	AY410029
34	590.8	24.9	667	7	CN315375	170004246
35	587.6	24.8	1182	1	AL528835	AL528835
36	585	24.6	680	4	BI761532	BI761532
37	578.6	24.4	940	5	BU049451	BU049451
38	573	24.1	584	1	BM253949	BM253949
39	571	24.1	740	1	AU117730	AU117730
40	568.2	23.9	658	5	BP152493	BP152493
41	566.8	23.9	789	5	B0852855	AGENCOURT
42	565.8	23.8	658	6	CA773784	CA773784
43	551.2	23.2	629	5	BX955707	DXFP781D
44	550.2	23.2	624	6	CB160361	CB160361
45	549.4	23.1	551	4	BM031987	497568 MA

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OW nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 6129.68 Seconds
(without alignment)
11448.874 Million cell updates/aec

Title: US-10-028-051A-3
Perfect score: 1484
Sequence: 1 cggggccctggggcgggaaggg.....acatgcgtgtaaaaaaaa 1484

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:
1: gb_ba:*
2: gb_hgt:*
3: gb_in:*
4: gb_co:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1473	99.3	1476	6	AX565712	AX565712 Sequence
2	1473	99.3	1476	6	AX597112	AX597112 Sequence
3	1473	99.3	1476	6	AX701367	AX701367 Sequence
4	1473	99.3	1476	6	AX821908	AX821908 Sequence
5	1473	99.3	1476	6	AX821908	AX821908 Sequence
6	1464.4	98.7	2039	6	AR129187	Sequence
7	1464.4	98.7	2039	6	AR447852	Sequence
8	1337	90.1	1363	9	BC027855	Homo sapi
9	1326.6	89.4	1920	6	BD192740	Secreted
10	1316.2	88.7	1893	6	AR116408	Endoderm,
11	1316.2	88.7	1893	6	BD195148	Endoderm,
12	1316.2	88.7	1893	9	HSU68057	Human fetal
13	1314.6	88.6	1909	6	AX329773	Sequence
14	1314.6	88.6	1909	6	AX329773	Sequence
15	1124.4	75.8	2351	4	BTU24164	AK130009
16	974.6	65.7	1687	9	AK130009	Homo sapi
17	860.6	58.0	2814	10	BC016884	Mus muscu
18	846.6	57.0	2540	10	MMU88568	Mus muscu
19	842.8	56.8	1786	10	MMU91905	Mus muscu
20	832.8	56.1	2176	6	AR116407	Endoderm,
21	832.8	56.1	2176	6	BD195147	Endoderm,
22	832.8	56.1	2176	6	AX305981	Sequence
23	832.8	56.1	2176	10	MMU68058	Mus muscu
24	670	45.1	97944	9	AC108514	Homo sapi
25	667	44.9	725	6	CQ719712	Sequence
26	660	44.5	1833	5	AF218057	Gallus ga
27	630.6	42.5	1076	10	MAU91904	Mesocricetu
28	483.4	32.6	487	6	CQ691410	Sequence
29	473.6	31.9	640	5	AF207665	Gallus ga
30	466.4	31.4	1291	5	XLU78598	Xenopus lae
31	466.2	31.4	1867	5	BC074538	Xenopus t
32	462	31.1	1875	5	U68059	Xenopus lae
33	462	31.1	1875	6	AR116405	Sequence
34	462	31.1	1875	6	BD195145	Endoderm,
35	452.6	30.5	472	6	CQ697461	Sequence
36	445.8	30.0	450	6	CQ683279	Sequence
37	436.6	29.4	190906	2	AL928578	Mouse DNA
38	436.6	29.4	250663	2	AC134905	Mus muscu
39	435.4	29.3	452	6	CQ685419	Sequence
40	434	29.2	611	11	BV099134	RPAMMSRQ

C	41	434	29.2	611	11	BV158572	BPV158572 RPAWSEQO
	42	423	28.5	1434	5	XLAV9304	AD009304 Xenopus 1
	43	419.6	28.3	238965	2	AC126647	AC126647 Rattus no
	44	412.4	27.8	427	6	CQ695880	CQ695880 Sequence
	45	410	27.6	124720	9	AC105396	AC105396 Homo sapi

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OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 647.611 Seconds
(without alignment)
12029.047 Million cell updates/sec

Title: US-10-028-051A-3

Perfect score: 1484
Sequence: 1 cgs9gacctgsgcgsgaagsg9g.....acatgctgtaaaaaaaaaa 1484

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
1: Geneseq1980a:*
2: Geneseq1990a:*
3: Geneseq2000a:*
4: Geneseq2001a:*
5: Geneseq2001ba:*
6: Geneseq2002a:*
7: Geneseq2002ba:*
8: Geneseq2003a:*
9: Geneseq2003ba:*
10: Geneseq2003ca:*
11: Geneseq2003da:*
12: Geneseq2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1483.6	100.0	1484	2	AAV18254 Human GRO
2	1473	99.3	1476	8	ABX75332 Human CDN
3	1473	99.3	1476	8	AAD52561 FRZB DNA.
4	1473	99.3	1476	8	AB281833 SARP-2 nu
5	1473	99.3	1476	10	ADK66946 Gene #36
6	1464.4	98.7	2039	4	AAF80535 Receptor
7	1464.4	98.7	2039	8	ABX77516 Different
8	1464.4	98.7	2039	12	ADL12749 Human ate
9	1326.6	89.4	1920	2	AAV28653 Nucleotid
10	1326.6	89.4	1920	3	AAA40573 Xenopus s
11	1316.2	88.6	1893	2	AAV14017 Human "fr
12	1314.6	88.6	1909	6	AAV13101 Human haf
13	1314.6	88.6	1909	6	AB161945 Colon ade
14	1314.6	88.6	1909	6	ABK64750 Human ben
15	1314.6	88.6	1909	10	ADL13671 Osteoarth
16	1314.6	88.6	1909	12	ADG20468 Human Fri

17	1314.6	88.6	1909	12	ADP21354	ADP21354 Gene FRZB
18	1124.4	75.8	2374	2	AAV18253	AAV18253 Bovine gr
19	976.4	65.8	978	10	ADL13672	ADL13672 Osteoarth
20	846.6	57.0	2540	12	ADG20470	ADG20470 Mouse Fir
21	844.8	56.9	2441	2	AAV13104	AAV13104 Mouse haf
22	842.8	56.8	1786	2	AAV13102	AAV13102 Mouse haf
23	832.8	56.1	2176	2	AAV14016	AAV14016 Mouse "fr
24	832.8	56.1	2176	6	AB199691	AB199691 Mouse ioc
25	630.6	42.5	1076	6	AAV13100	AAV13100 Hamster B
26	470.2	31.7	476	6	ABK64764	ABK64764 Human ben
27	466.4	31.4	1291	2	AAV18255	AAV18255 Xenopus g
28	462	31.1	1875	2	AAV14014	AAV14014 Xenopus "
29	435.6	29.4	475	9	ACH13647	ACH13647 Human adu
30	419.6	28.3	5301	2	AAV13105	AAV13105 Mouse haf
31	419.6	28.3	5355	2	AAV13103	AAV13103 Mouse haf
32	407.2	27.4	489	9	ACH28855	ACH28855 Human adu
33	392.6	19.7	1041	3	AAV98046	AAV98046 Bos tauru
34	289.4	19.5	1458	2	AAV08951	AAV08951 Human ATG
35	289.4	19.5	1988	9	ADA24512	ADA24512 Human CDN
36	289.4	19.5	2009	4	AAF80598	AAF80598 Receptor
37	288.8	19.5	2819	8	AAD52571	AAD52571 SRFP 4 DN
38	287.8	19.4	1046	2	AAV28655	AAV28655 Nucleotid
39	287.8	19.4	1581	2	AAV28656	AAV28656 Full leng
40	287.8	19.4	1767	4	AAV08495	AAV08495 Human FRA
41	286.2	19.3	1041	3	AAA54128	AAA54128 Breast ca
42	286.2	19.3	1767	2	AAV08057	AAV08057 Human FRA
43	286.2	19.3	2820	6	ABK92118	ABK92118 Prostate
44	286.2	19.3	2820	8	ABZ34846	ABZ34846 Coding se
45	286.2	19.3	2820	8	ABX76341	ABX76341 Lung canc

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OM nucleic - nucleic search, using sw model
Run on: January 10, 2005, 11:50:10 ; Search time 130.56 Seconds
(without alignment)
8079.143 Million cell updates/sec

Title: US-10-028-051A-3
Perfect score: 1484
Sequence: 1 cgs9gacctgsgcgsgaagsg9g.....acatgctgtaaaaaaaaaa 1484

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/6C_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/6D_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query
--------	-------

No.	Score	Match Length	DB	ID	Description
1	1464.4	98.7	2039	3	US-09-276-531-45
2	1464.4	98.7	2039	4	US-09-976-594-478
3	1316.2	88.7	1893	3	US-08-878-474-10
4	832.8	56.1	2176	3	US-08-878-474-8
5	462	31.1	1875	3	US-08-878-474-4
6	289.4	19.5	2009	3	US-09-276-531-108
7	235	15.8	246	4	US-09-016-434-103
8	64	4.3	401	4	US-09-643-597-277
9	64	4.3	401	4	US-09-480-884A-277
10	64	4.3	401	4	US-09-542-615A-277
11	64	4.3	401	4	US-09-606-421B-277
12	64	4.3	401	4	US-09-630-940B-277
13	61.4	4.1	588	4	US-09-546-043-10
14	61.4	4.1	1984	4	US-08-937-067-5
15	59	4.0	741	4	US-09-546-043-11
16	59	4.0	804	4	US-09-546-043-12
17	59	4.0	942	4	US-09-546-043-2
18	59	4.0	1017	4	US-09-546-043-9
19	59	4.0	2075	4	US-09-087-031E-2
20	59	4.0	2075	4	US-09-546-043-1
21	59	4.0	2078	4	US-09-087-031E-1
22	59	4.0	2078	4	US-09-514-885-2
23	59	4.0	4245	3	US-09-276-531-16
24	59	4.0	4500	4	US-09-087-031E-27
25	57.4	3.9	1308	4	US-08-937-067-18
26	51.8	3.5	1869	4	US-09-148-545-56
27	51.2	3.5	870	4	US-08-937-067-3
28	51.2	3.5	1960	4	US-09-148-545-114
29	49	3.3	2030	4	US-08-937-067-1
30	46.8	3.2	6090	4	US-09-631-603-1
31	45.8	3.1	7218	1	US-08-232-463-14
32	45.2	3.0	546	4	US-09-252-991A-6912
33	45.2	3.0	1197	4	US-09-252-991A-6912
34	45.2	3.0	1272	4	US-09-252-991A-6952
35	45.2	3.0	2346	4	US-09-252-991A-6782
36	44.6	3.0	2124	4	US-09-087-031E-26
37	43	2.9	711	4	US-09-252-991A-5727
38	43	2.9	765	4	US-09-252-991A-15854
39	43	2.9	1548	4	US-09-252-991A-5713
40	43	2.9	1971	4	US-09-252-991A-5699
41	43	2.9	2265	4	US-09-252-991A-5738
42	42.8	2.9	2310	3	US-08-956-182-13
43	42.8	2.9	7218	1	US-08-232-463-14
44	42.4	2.9	1446	4	US-09-252-991A-10586
45	42.4	2.9	3222	4	US-09-252-991A-10770

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OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 1411.66 Seconds
(without alignment)
6031.844 Million cell updates/sec

Title: US-10-028-051A-3
Perfect score: 1484
Sequence: 1 CGGGGCGCTGGGCGGAGGGGG.....acatgctgtaaaaaaaaaa 1484

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4293498 seqs, 2868903791 residues

Total number of hits satisfying chosen parameters: 8586996

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

- 1: /cgm2_6/ptodata/1/pub/pna/US07_PUBCOMB.seq:*
- 2: /cgm2_6/ptodata/1/pub/pna/PCT_NEW_PUB.seq:*
- 3: /cgm2_6/ptodata/1/pub/pna/US06_NEW_PUB.seq:*
- 4: /cgm2_6/ptodata/1/pub/pna/US06_PUBCOMB.seq:*
- 5: /cgm2_6/ptodata/1/pub/pna/US07_NEW_PUB.seq:*
- 6: /cgm2_6/ptodata/1/pub/pna/PCUS_PUBCOMB.seq:*
- 7: /cgm2_6/ptodata/1/pub/pna/US08_NEW_PUB.seq:*
- 8: /cgm2_6/ptodata/1/pub/pna/US08_PUBCOMB.seq:*
- 9: /cgm2_6/ptodata/1/pub/pna/US09A_PUBCOMB.seq:*
- 10: /cgm2_6/ptodata/1/pub/pna/US09B_PUBCOMB.seq:*
- 11: /cgm2_6/ptodata/1/pub/pna/US09C_PUBCOMB.seq:*
- 12: /cgm2_6/ptodata/1/pub/pna/US09_NEW_PUB.seq:*
- 13: /cgm2_6/ptodata/1/pub/pna/US10_PUBCOMB.seq:*
- 14: /cgm2_6/ptodata/1/pub/pna/US10C_PUBCOMB.seq:*
- 15: /cgm2_6/ptodata/1/pub/pna/US10D_PUBCOMB.seq:*
- 16: /cgm2_6/ptodata/1/pub/pna/US10E_PUBCOMB.seq:*
- 17: /cgm2_6/ptodata/1/pub/pna/US10F_PUBCOMB.seq:*
- 18: /cgm2_6/ptodata/1/pub/pna/US11_NEW_PUB.seq:*
- 19: /cgm2_6/ptodata/1/pub/pna/US11_NEW_PUB.seq:*
- 20: /cgm2_6/ptodata/1/pub/pna/US60_NEW_PUB.seq:*
- 21: /cgm2_6/ptodata/1/pub/pna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
1	1483.6	100.0	1484	13	US-10-028-051-3
2	1483.6	100.0	1484	14	US-10-090-049-3
3	1483.6	100.0	1484	15	US-10-014-055-3
4	1473	99.3	1476	15	US-10-172-118-614
5	1473	98.3	1476	16	US-10-342-887-614
6	1464.4	99.7	2039	9	US-09-974-298-16
7	1427.2	96.2	2625	16	US-10-062-674-1395
8	1316.2	88.7	1893	9	US-09-903-180B-10
9	1316.2	88.7	1893	9	US-09-903-187A-10
10	1316.2	88.7	1893	9	US-09-903-171A-10
11	1316.2	88.7	1893	9	US-09-903-188A-10
12	1316.2	88.7	1893	9	US-09-903-323A-10
13	1316.2	88.7	1893	9	US-09-903-325A-10
14	1316.2	88.6	1893	9	US-09-903-170C-10
15	1314.6	88.6	1909	10	US-09-960-706-989
16	1314.6	88.6	1909	10	US-09-873-319-645
17	1314.6	88.6	1909	10	US-09-873-367C-282
18	1124.4	75.8	2374	13	US-10-028-051-1
19	1124.4	75.8	2374	14	US-10-090-049-1
20	1124.4	75.8	2374	15	US-10-014-055-1
21	832.8	56.1	2176	9	US-09-903-180B-8
22	832.8	56.1	2176	9	US-09-903-187A-8
23	832.8	56.1	2176	9	US-09-903-171A-8
24	832.8	56.1	2176	9	US-09-903-188A-8
25	832.8	56.1	2176	9	US-09-903-323A-8
26	832.8	56.1	2176	9	US-09-903-325A-8
27	832.8	56.1	2176	9	US-09-903-170C-8
28	483.4	32.6	487	16	US-10-242-535A-36336
29	483.4	32.6	487	16	US-10-085-783A-36336
30	470.2	31.7	476	10	US-09-960-706-1006
31	470.2	31.7	476	10	US-09-873-319-659
32	466.4	31.4	1291	13	US-10-028-051-23
33	466.4	31.4	1291	14	US-10-090-049-23
34	466.4	31.4	1291	15	US-10-014-055-23
35	462	31.1	1875	9	US-09-903-180B-4
36	462	31.1	1875	9	US-09-903-187A-4
37	462	31.1	1875	9	US-09-903-171A-4
38	462	31.1	1875	9	US-09-903-188A-4

39	462	31.1	1875	9	US-09-903-323A-4	Sequence 4, Appli
40	462	31.1	1875	9	US-09-903-325A-4	Sequence 4, Appli
41	462	31.1	1875	9	US-09-903-170C-4	Sequence 4, Appli
42	452.6	30.5	472	16	US-10-242-535A-42387	Sequence 42387, A
43	452.6	30.5	472	16	US-10-085-783A-42387	Sequence 42387, A
44	445.8	30.0	450	16	US-10-242-535A-28205	Sequence 28205, A
45	445.8	30.0	450	16	US-10-085-783A-28205	Sequence 28205, A

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OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 4234.4 Seconds
(without alignments)
12770.772 Million cell updates/sec

Title: US-10-028-051A-3
Perfect score: 1484
Sequence: 1 cggggcctggggcgagggg.....acatgctgttaaaaaaaaaa 1484

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 1821965908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
- 1: gb_eet1.*
 - 2: gb_eet2.*
 - 3: gb_htc.*
 - 4: gb_eet3.*
 - 5: gb_eet4.*
 - 6: gb_eet5.*
 - 7: gb_eet6.*
 - 8: gb_gse1.*
 - 9: gb_gse2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1330.2	89.6	1891	3	CR622855 full-leng
2	1298	87.5	1305	3	CR593578 full-leng
3	1259.2	84.9	1780	3	CR620343 full-leng
4	1040.6	70.1	1159	1	AL515416 AL515416
5	1014.2	68.3	1065	7	U69182 U69182
6	963.2	64.9	1051	1	AL573040 AL573040
7	939.8	63.3	1094	1	AL528836 AL528836
8	937.4	63.2	1032	1	AL546734 AL546734
9	923.6	62.2	1001	1	AL548498 AL548498
10	875.6	59.0	991	1	AL526385 AL526385
11	871.4	58.7	928	1	AL527859 AL527859
12	861.4	58.0	2390	3	AK019093 Mus muscu
13	861.4	58.0	2922	3	AK029941 Mus muscu
14	814.4	54.9	891	6	CD105319 AGENCOURT
15	766.2	51.6	781	5	BQ044934 UI-H-EUO-
16	754.2	50.8	1043	5	BX459201 BX459201
17	749	50.5	797	9	AYA10028 Homo sapi

c	18	739	49.8	762	5	BQ182099
c	19	737.2	49.7	835	4	B1913036
c	20	731	49.3	739	5	BQ006836
c	21	730.4	49.2	789	5	B0852855
c	22	728	49.1	737	5	B0733641
c	23	725.4	48.9	787	1	AU141161
c	24	718	48.4	728	4	B1832471
c	25	713.2	48.1	805	4	B1769191
c	26	709	47.8	719	7	CN315376
c	27	700.8	47.2	712	5	BX955693
c	28	681.4	45.9	708	1	A1075764
c	29	676.6	45.6	740	1	AU117730
c	30	666.8	44.9	797	9	AY410029
c	31	665.6	44.9	693	5	B0732915
c	32	661.6	44.6	678	2	AW160750
c	33	659.8	44.5	695	1	A1983481
c	34	659	44.4	667	7	CN315375
c	35	653.8	44.1	680	4	B1761532
c	36	635.6	42.8	658	6	CA773784
c	37	632.2	42.6	797	9	AY410030
c	38	627.2	42.3	653	4	B0706252
c	39	625.8	42.2	745	5	BP148017
c	40	625	42.1	730	5	BP147378
c	41	624.6	42.1	705	2	AW955823
c	42	624.4	42.1	642	4	B1711161
c	43	616.2	41.5	629	5	BX955707
c	44	612	41.2	624	6	CB160361
c	45	610	41.1	641	4	B1668012

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OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 5332.49 Seconds
(without alignments)
11448.874 Million cell updates/sec

Title: US-10-028-051A-23

Perfect score: 1291
Sequence: 1 tttaactgtgcagctctccc.....agcctatcatctgataccta 1291

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :	GenEmbl:*
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2:	gb_hcg:*
3:	gb_in:*
4:	gb_om:*
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6:	gb_pat:*
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8:	gb_pl:*
9:	gb_pr:*
10:	gb_ro:*
11:	gb_sts:*
12:	gb_ay:*
13:	gb_un:*
14:	gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1291	100.0	1291	5	XLU78598	U78598 Xenopus lae
2	1131.6	87.7	1875	5	U68059	U68059 Xenopus lae
3	1131.6	87.7	1875	6	AR116405	AR116405 Sequence
4	1131.6	87.7	1875	6	BD195145	BD195145 Endoderm,
5	1028.2	79.6	1867	5	BC074538	BC074538 Xenopus t
6	992.4	76.9	1434	5	XLAU9304	XLAU9304 Xenopus l
7	518	40.1	1833	5	AF218057	AF218057 Gallus ga
8	468	36.3	1920	6	BD192740	BD192740 Secreted
9	466.4	36.1	1363	9	BC027855	BC027855 Homo sapi
10	466.4	36.1	1893	6	AR116408	AR116408 Sequence
11	466.4	36.1	1893	9	BD195148	BD195148 Endoderm,
12	466.4	36.1	1893	9	HSU68057	HSU68057 Human firez
13	466.4	36.1	2039	6	AR129187	AR129187 Sequence
14	466.4	36.1	2039	6	AR447852	AR447852 Sequence
15	464.8	36.0	1476	6	AX565712	AX565712 Sequence
16	464.8	36.0	1476	6	AX597112	AX597112 Sequence
17	464.8	36.0	1476	6	AX701367	AX701367 Sequence
18	464.8	36.0	1476	6	AX821908	AX821908 Sequence
19	464.8	36.0	1476	9	HSU24163	HSU24163 Human Frlz
20	464.8	36.0	1909	9	AX329773	AX329773 Sequence
21	464.8	36.0	1909	9	HSU91903	HSU91903 Human Frlz
22	463.6	35.9	2814	10	BCU16884	BCU16884 Mus muscu
23	462	35.8	1786	10	MMU91905	MMU91905 Mus muscu
24	462	35.8	2176	6	AR116407	AR116407 Sequence
25	462	35.8	2176	6	BD195147	BD195147 Endoderm,
26	462	35.8	2176	6	AX305981	AX305981 Sequence
27	462	35.8	2176	10	MMU68058	MMU68058 Mus muscu
28	462	35.8	2540	10	MMU88568	MMU88568 Mus muscu
29	452	35.0	2351	4	BTU24164	BTU24164 Bos taurus
30	394.6	30.6	948	5	AF116853	AF116853 Danio rer
31	373.6	28.9	1076	10	MAU91904	MAU91904 Mesocricetu
32	373.4	28.9	640	5	AF207665	AF207665 Gallus ga
33	345.6	26.8	725	6	CQ719712	CQ719712 Sequence
34	283.6	22.0	1687	9	AK130009	AK130009 Homo sapi
35	266.6	20.7	1785	10	AF117709	AF117709 Mus muscu
36	263.4	20.4	1739	10	BC034853	BC034853 Mus muscu
37	259.8	20.1	97944	9	AC108514	AC108514 Homo sapi
38	258.6	20.0	19096	10	AL928578	AL928578 Mouse DNA
39	258.6	20.0	238965	2	AC126647	AC126647 Rattus no
40	258.6	20.0	250663	2	AC134905	AC134905 Mus muscu
41	257.2	19.9	611	11	BV099134	BV099134 RPAWMSQ
42	257.2	19.9	611	11	BV158572	BV158572 RPAWMSQ
43	251.8	19.5	1910	10	AF012891	AF012891 Rattus no
44	250.8	19.4	1715	10	AF140346	AF140346 Rattus no
45	247.6	19.2	162126	2	CR513785	CR513785 Danio rer

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OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 563.386 Seconds
(without alignment)
12029.047 Million cell updates/sec

Title: US-10-028-051A-23

Perfect score: 1291
Sequence: 1 ttctactgtgcagctctccc.....agcctatcattgcactca 1291

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134866 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :	N_Geneseq_23Sep04:*
1:	geneseq11960a:*
2:	geneseq11990a:*
3:	geneseq2000a:*
4:	geneseq2001a:*
5:	geneseq2001b:*
6:	geneseq2002a:*
7:	geneseq2002b:*
8:	geneseq2003a:*
9:	geneseq2003b:*
10:	geneseq2003c:*
11:	geneseq2003d:*
12:	geneseq2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1291	100.0	1291	2	AAV18255	AAV18255 Xenopus g
2	1131.6	87.7	1875	2	AAV14014	AAV14014 Xenopus "
3	468	36.3	1920	2	AAx28653	AAx28653 Nucleotid
4	468	36.3	1920	3	AAA40573	AAA40573 Xenopus g
5	466.4	36.1	1484	2	AAV18254	AAV18254 Human gro
6	466.4	36.1	1893	2	AAV14017	AAV14017 Human "fr
7	466.4	36.1	2039	4	AAE80535	AAE80535 Receptor
8	466.4	36.1	2039	8	ABX77516	ABX77516 Different
9	466.4	36.1	2039	12	ADL12749	ADL12749 Human ste
10	464.8	36.0	1476	8	ABX75332	ABX75332 Human CDN
11	464.8	36.0	1476	8	AAD52561	AAD52561 FRZB DNA.
12	464.8	36.0	1476	8	ABZ81833	ABZ81833 SARP-2 nu
13	464.8	36.0	1476	10	ADK66946	ADK66946 Gene #36
14	464.8	36.0	1909	2	AAV13101	AAV13101 Human hnf
15	464.8	36.0	1909	6	ABL61945	ABL61945 Colon ade
16	464.8	36.0	1909	6	ABK64750	ABK64750 Human ben
17	464.8	36.0	1909	10	ADL13671	ADL13671 Osteoarth
18	464.8	36.0	1909	12	ADP21354	ADP21354 Gene FRZB
19	464.8	36.0	1909	12	ADP21354	ADP21354 Gene FRZB
20	462	35.8	1786	2	AAV13102	AAV13102 Mouse hnf
21	462	35.8	2176	6	ABV14016	ABV14016 Mouse "fr
22	462	35.8	2176	6	ABV19691	ABV19691 Mouse iac
23	462	35.8	2441	2	AAV13104	AAV13104 Mouse hnf
24	462	35.8	2540	12	ADG20470	ADG20470 Mouse Frl
25	459.8	35.6	978	10	ADL13672	ADL13672 Osteoarth
26	452	35.0	2374	2	AAV18253	AAV18253 Bovine gr
27	373.6	28.9	1076	2	AAV13100	AAV13100 Hamster B
28	321.6	24.9	352	3	AAA43168	AAA43168 Xenopus g
29	245.8	19.0	5301	2	AAV13105	AAV13105 Mouse hnf
30	245.8	19.0	5355	2	AAV13103	AAV13103 Mouse hnf
31	244.2	18.9	1458	2	AAV08951	AAV08951 Human ATG
32	244.2	18.9	1988	9	ADA24512	ADA24512 Human CDN
33	244.2	18.9	2009	4	AAF80598	AAF80598 Receptor
34	241	18.7	1041	3	AAA54128	AAA54128 Breast ca
35	241	18.7	1046	2	AAx28655	AAx28655 Nucleotid
36	241	18.7	1581	2	AAx28656	AAx28656 Full leng
37	241	18.7	1767	2	AAV80657	AAV80657 Human FRA
38	241	18.7	1767	4	AAc84495	AAc84495 Human FRA
39	241	18.7	2820	6	ABK92118	ABK92118 Prostate
40	241	18.7	2820	8	ABZ34846	ABZ34846 Coding se

41 241 18.7 2820 8 ABX76341 ABX76341 Lung canc
42 241 18.7 2820 8 ABX75341 ABX75341 Human cDN
43 241 18.7 2820 8 ABX281843 ABX281843 SRFP-1 nu
44 241 18.7 2820 11 ADN38745 ADN38745 Cancer/an
45 241 18.7 2820 11 ADN39642 ADN39642 Cancer/an

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OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 113.58 Seconds
(without alignments)
8079.143 Million cell updates/sec

Title: US-10-028-051A-23

Perfect score: 1291

Sequence: 1 ttaccgtgcagctctccc.....agccatcatctgataccta 1291

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patente_NA:*
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5: /cgm2_6/ptodata/1/ina/PCRTUS_COMB.seq:*
6: /cgm2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
	1	1131.6	87.7	1875	3	US-08-878-474-4 Sequence 4, Appl1
	2	466.4	36.1	1893	3	US-08-878-474-10 Sequence 10, Appl1
	3	466.4	36.1	2039	3	US-09-276-531-45 Sequence 45, Appl1
	4	466.4	36.1	2039	4	US-09-276-531-45 Sequence 478, Appl1
	5	462	35.8	2176	3	US-08-878-474-8 Sequence 8, Appl1
	6	244.2	18.9	2009	3	US-09-276-531-108 Sequence 108, Appl1
	7	107.6	8.3	246	4	US-09-016-434-103 Sequence 103, Appl1
	8	70	5.4	401	4	US-09-643-597-277 Sequence 277, Appl1
	9	70	5.4	401	4	US-09-480-884A-277 Sequence 277, Appl1
	10	70	5.4	401	4	US-09-542-615A-277 Sequence 277, Appl1
	11	70	5.4	401	4	US-09-606-421B-277 Sequence 277, Appl1
	12	70	5.4	401	4	US-09-630-940B-277 Sequence 277, Appl1
	13	56.6	4.4	1796	3	US-09-276-531-113 Sequence 113, Appl1
	14	49.6	3.8	7218	1	US-08-232-463-14 Sequence 22, Appl1
	15	42.4	3.3	1141	4	US-09-806-708B-22 Sequence 114, Appl1
	16	35.6	2.8	1960	4	US-08-545-528D-1 Sequence 2813, Appl1
	17	35.4	2.7	580073	4	US-09-621-976-2813 Sequence 5, Appl1
	18	35.2	2.7	832	4	US-09-031-962D-5 Sequence 31, Appl1
	19	35	2.7	1109	4	US-06-256-204C-31 Sequence 56, Appl1
	20	35	2.7	1109	4	US-09-148-545-56 Sequence 56, Appl1
	21	35	2.7	1109	4	US-09-148-545-56 Sequence 56, Appl1
	22	35	2.7	1109	4	US-09-148-545-56 Sequence 56, Appl1

23	34.6	2.7	3436	4	US-09-919-039-277 Sequence 277, Appl1
24	34.6	2.7	4069	4	US-09-620-312D-174 Sequence 174, Appl1
25	34.6	2.7	202001	4	US-09-734-674-3 Sequence 3, Appl1
26	34.4	2.7	561	4	US-09-248-796A-4855 Sequence 4855, Appl1
27	34.2	2.6	1984	4	US-08-937-067-5 Sequence 5, Appl1
28	34.2	2.6	2565	3	US-08-985-492-7 Sequence 7, Appl1
29	34.2	2.6	3026	4	US-09-919-039-314 Sequence 314, Appl1
30	34.2	2.6	8050	3	US-09-491-362-11 Sequence 11, Appl1
31	34.2	2.6	8050	4	US-09-874-562-11 Sequence 11, Appl1
32	34.2	2.6	1830121	4	US-09-557-884-1 Sequence 1, Appl1
33	34.2	2.6	1830121	4	US-09-643-990A-1 Sequence 1, Appl1
34	34.2	2.6	1830121	4	US-10-329-960-1 Sequence 1, Appl1
35	34	2.6	1287	3	US-08-845-258-11 Sequence 11, Appl1
36	34	2.6	1287	3	US-08-990-571-11 Sequence 11, Appl1
37	34	2.6	1287	3	US-08-723-142A-11 Sequence 11, Appl1
38	34	2.6	1287	4	US-09-528-784A-11 Sequence 11, Appl1
39	34	2.6	1287	4	US-09-569-098A-11 Sequence 11, Appl1
40	34	2.6	7218	1	US-08-232-463-14 Sequence 14, Appl1
41	33.8	2.6	168575	4	US-09-426-290-1 Sequence 1, Appl1
42	33.6	2.6	475	4	US-09-621-976-909 Sequence 909, Appl1
43	33.6	2.6	501	4	US-09-328-352-439 Sequence 439, Appl1
44	33.6	2.6	621	4	US-09-248-796A-7246 Sequence 7246, Appl1
45	33.4	2.6	664	4	US-09-904-615-66 Sequence 66, Appl1

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OM nucleic - nucleic search, using sw model

Run on: January 10, 2005, 11:50:10 ; Search time 1228.07 Seconds
(without alignments)
6031.844 Million cell updates/sec

Title: US-10-028-051A-23
Perfect score: 1291
Sequence: 1 ttaccgtgcagctctccc.....agccatcatctgataccta 1291

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4293498 seqs, 2868903791 residues

Total number of hits satisfying chosen parameters: 8586996

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgm2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgm2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
7: /cgm2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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10: /cgm2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgm2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgm2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgm2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgm2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
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20: /cgm2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

21: /cgn2_6/ptodata/1/pub/pna/US60_FUBCOMB.seq:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result					Description				
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1	1291	100.0	1291	13	US-10-028-051-23	Sequence 23, Appl			
2	1291	100.0	1291	14	US-10-090-049-23	Sequence 23, Appl			
3	1291	100.0	1291	15	US-10-014-055-23	Sequence 23, Appl			
4	1131.6	87.7	1875	9	US-09-903-180B-4	Sequence 4, Appl			
5	1131.6	87.7	1875	9	US-09-903-187A-4	Sequence 4, Appl			
6	1131.6	87.7	1875	9	US-09-903-171A-4	Sequence 4, Appl			
7	1131.6	87.7	1875	9	US-09-903-188A-4	Sequence 4, Appl			
8	1131.6	87.7	1875	9	US-09-903-323A-4	Sequence 4, Appl			
9	1131.6	87.7	1875	9	US-09-903-325A-4	Sequence 4, Appl			
10	1131.6	87.7	1875	9	US-09-903-170C-4	Sequence 4, Appl			
11	466.4	36.1	1484	13	US-10-028-051-3	Sequence 3, Appl			
12	466.4	36.1	1484	14	US-10-090-049-3	Sequence 3, Appl			
13	466.4	36.1	1484	15	US-10-014-055-3	Sequence 3, Appl			
14	466.4	36.1	1893	9	US-09-903-180B-10	Sequence 10, Appl			
15	466.4	36.1	1893	9	US-09-903-187A-10	Sequence 10, Appl			
16	466.4	36.1	1893	9	US-09-903-171A-10	Sequence 10, Appl			
17	466.4	36.1	1893	9	US-09-903-188A-10	Sequence 10, Appl			
18	466.4	36.1	1893	9	US-09-903-323A-10	Sequence 10, Appl			
19	466.4	36.1	1893	9	US-09-903-325A-10	Sequence 10, Appl			
20	466.4	36.1	1893	9	US-09-903-170C-10	Sequence 10, Appl			
21	466.4	36.1	2039	9	US-09-974-298-16	Sequence 16, Appl			
22	466.4	36.1	2625	16	US-10-062-674-1395	Sequence 1395, Ap			
23	464.8	36.0	1476	15	US-10-172-118-614	Sequence 614, App			
24	464.8	36.0	1476	16	US-10-342-887-614	Sequence 989, App			
25	464.8	36.0	1909	10	US-09-960-706-989	Sequence 645, App			
26	464.8	36.0	1909	10	US-09-873-319-645	Sequence 282, App			
27	464.8	36.0	1909	10	US-09-873-367C-282	Sequence 8, Appl			
28	462	35.8	2176	9	US-09-903-180B-8	Sequence 8, Appl			
29	462	35.8	2176	9	US-09-903-187A-8	Sequence 8, Appl			
30	462	35.8	2176	9	US-09-903-171A-8	Sequence 8, Appl			
31	462	35.8	2176	9	US-09-903-188A-8	Sequence 8, Appl			
32	462	35.8	2176	9	US-09-903-323A-8	Sequence 8, Appl			
33	462	35.8	2176	9	US-09-903-325A-8	Sequence 8, Appl			
34	462	35.8	2176	9	US-09-903-170C-8	Sequence 8, Appl			
35	452	35.0	2374	13	US-10-028-051-1	Sequence 1, Appl			
36	452	35.0	2374	14	US-10-090-049-1	Sequence 1, Appl			
37	452	35.0	2374	15	US-10-014-055-1	Sequence 1, Appl			
38	244.2	18.9	1988	16	US-10-208-408-28	Sequence 28, Appl			
39	241	18.7	1443	16	US-10-610-917-1	Sequence 1, Appl			
40	241	18.7	1581	16	US-10-610-917-3	Sequence 3, Appl			
41	241	18.7	2820	15	US-10-301-822-188	Sequence 188, App			
42	241	18.7	2820	15	US-10-285-027-63	Sequence 63, Appl			
43	241	18.7	2820	15	US-10-295-027-960	Sequence 960, App			
44	241	18.7	2820	18	US-10-473-974-204	Sequence 204, App			
45	241	18.7	2839	9	US-09-909-775-1	Sequence 1, Appl			

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OM nucleic - nucleic search, using nw model

Run on: January 10, 2005, 11:50:10 ; Search time 3683.7 Seconds
(without alignment)
12770.772 Million cell updates/sec

Title: US-10-028-051A-23
Perfect score: 1291
Sequence: 1 ttactgtgcagctctccc.....agcctatcatcgtacacta 1291

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 33822875 seqs, 18219865908 residues
Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result					Description				
No.	Score	Query	Match	Length	DB	ID			
1	770.6	59.7	851	5	B0908005	B0908005	AGENCOURT		
2	698.6	54.1	885	6	CA988026	CA988026	AGENCOURT		
3	662.6	51.3	923	5	B0906569	B0906569	AGENCOURT		
4	592.2	45.9	702	5	BX853989	BX853989	AGENCOURT		
5	524.2	40.6	745	6	CF284632	CF284632	AGENCOURT		
6	495.2	38.4	736	7	CK653921	CK653921	AGENCOURT		
7	480.6	37.2	929	5	BX755490	BX755490	AGENCOURT		
8	466.4	36.1	1305	3	CR593578	CR593578	full-leng		
9	466.4	36.1	1780	3	CR620343	CR620343	full-leng		
10	466.4	36.1	1891	3	CR622855	CR622855	full-leng		
11	462	35.8	2390	3	AK019093	AK019093	Mus muscu		
12	462	35.8	2922	3	AK029941	AK029941	Mus muscu		
13	453.6	35.1	1001	1	AL548498	AL548498	AL548498		
14	451.4	35.0	1032	1	AL546734	AL546734	AL546734		
15	447.6	34.7	1159	1	AL515416	AL515416	AL515416		
16	446.6	34.6	940	5	BU409451	BU409451	603157994		
17	434.6	33.7	882	5	BX758011	BX758011	BM758011		
18	430	33.3	891	6	CD105319	CD105319	AGENCOURT		
19	423.4	32.8	1094	1	AL528836	AL528836	AL528836		
20	418.2	32.4	835	5	BU910785	BU910785	AGENCOURT		
21	418.2	32.4	960	7	CF591381	CF591381	AGENCOURT		
22	411.2	31.9	928	1	AL527859	AL527859	AL527859		
23	409.8	31.7	688	4	BT618816	BT618816	BT618816		
24	396.2	30.7	1700	6	CB417263	CB417263	STR00740		
25	393.6	30.5	797	9	AY410030	AY410030	Mus muscu		
26	392	30.4	797	9	AY410028	AY410028	Homo sapi		
27	377.4	29.2	482	1	AL800329	AL800329	AL800329		
28	372.8	28.9	750	6	CF284609	CF284609	AGENCOURT		
29	365.2	28.3	797	6	CF284587	CF284587	AGENCOURT		
30	357.8	27.7	649	4	BT033833	BT033833	BT033833		
31	357.8	27.7	651	4	BT625268	BT625268	BT625268		
32	354.4	27.5	1065	7	U69182	U69182	Soar		
33	353.6	27.4	759	7	CN083539	CN083539	EC2BBA22D		
34	353.6	27.4	805	4	BT769191	BT769191	603060007		
35	349.4	27.1	910	6	CN325999	CN325999	AGENCOURT		
36	349	27.0	910	6	CF220920	CF220920	AGENCOURT		
37	348.6	27.0	651	2	AW318973	AW318973	un10B10..Y		
38	348	27.0	991	1	AL526385	AL526385	AL526385		
39	346.6	26.8	797	9	AY410029	AY410029	Pan trogl		

C	40	345.2	26.7	792	5	BX762262	BX762262
	41	343.8	26.6	889	7	COS58209	AGENCOURT
	42	342	26.5	1043	5	BX459201	BX459201
	43	337.2	26.1	787	1	AU141161	AU141161
	44	334.6	25.9	678	2	AW160750	au75f01.y
	45	332.6	25.8	680	4	BI761532	BI761532 603046682